

1/31

	1		50
EG327	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA SATVATAVLA TLLFATVQAS.
BZ198	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA SATVATAVLA TLLFATVQAN
BZ10	MNKISRIIWN	SALNAWVVVS	ELTRNHTKRA SATVATAVLA TLLFATVQAN
H15	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA SATVATAVLA TLLFATVQAN
EG329	MNEILRIIWN	SALNAWVVVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAS
PMC21	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAS
H38	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAN
P20	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA SATVATAVLA TLLSATVQAN
Z2491	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAN
H41	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAN
Consensus	<u>MN-I-RIIWN</u>	<u>SALNAW-VS</u>	<u>ELTRNHTKRA SATV-TAVLA TLL-ATVQA-</u>

C1

	51		100
EG327	TTDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.VTED SNWGVYFDKK
BZ198	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
BZ10	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
H15	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
EG329	ANNEEQEEDL	YLDPVLRIVA	VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
PMC21	ANNEEQEEDL	YLDPVQRTVA	VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
H38	ATDED...EEE	ELEPVRSAL	VLQFMIDKEG NGENE.STGN IGWSIYYDNH
P20	ATDTD...EDE	ELESVARSA	VLQFMIDKEG NGEIESTGDI GWSIYYDDHN
Z2491	ATDED...EEE	ELESVQR.SV	VGSIQASMEG SGELET...I SLSMTNDSKE
H41	ATDED...EEE	ELESVQR.SV	VGSIQASMEG SVELET...I SLSMTNDSKE
Consensus	-----	-L--V-R--	V-----EG --E-E-----

V1

	101		150
EG327	GVLTAGTITL	KAGDNLKIQ	NTNENTNASSFTYSLK KDLTDLTSVG
BZ198	RVLKAGAITL	KAGDNLKIQ	NTNENTNDSSFTYSLK KDLTDLTSVE
BZ10	RVLKAGAITL	KAGDNLKIQ	NTNENTNENT NDSSFTYSLK KDLTDLTSVE
H15	RVLKAGAITL	KAGDNLKIQ	NTNENTNENT NDSSFTYSLK KDLTDLTSVE
EG329	GVLTAAREITL	KAGDNLKIQ	NG...TN...FTYSLK KDLTDLTSVG
PMC21	GVLTAAREITL	KAGDNLKIQ	NG...TN...FTYSLK KDLTDLTSVG
H38	NTLHGATVTL	KAGDNLKIQ	NTNKNTNENT NDSSFTYSLK KDLTDLTSVE
P20	TLHG.ATVTL	KAGDNLKIQ	SGKD.....FTYSLK KELKDLTSVE
Z2491	FVDPYIVVTL	KAGDNLKIQ	NTNENTNASSFTYSLK KDLTGILNVE
H41	FVDPYIVVTL	KAGDNLKIQ	NTNENTNASSFTYSLK KDLTGILNVE
Consensus	-----	<u>TL KAGDNLKIQ</u>	-----FTYSLK K-L--L--V-

V1

C2

V2

C3

FIG. 1A



2/31

	151		200
EG327	TEKLSFSANS NKVNITSDTK GLNFAKKTAE	TNGDPTVHLN	GIGSTLTDTL
BZ198	TEKLSFGANG NKVNITSDTK GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
BZ10	TEKLSFGANG NKVNITSDTK GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
H15	TEKLSFGANG NKVNITSDTK GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
EG329	TEKLSFSANG NKVNITSDTK GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
PMC21	TEKLSFSANG NKVNITSDTK GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
H38	TEKLSFGANG NKVNITSDTK GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
P20	TEKLSFGANG NKVNITSDTK GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
Z2491	TEKLSFGANG KKVNIISDTK GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
H41	TEKLSFGANG KKVNIISDTK GLNFAKETAG	TNGDPTVHLN	GIGSTLTDM
Consensus	<u>TEKLSF-AN- -KVNI-SDTK GLNFAK-TA- TNGD-TVHLN</u>	<u>GIGSTLTDL-L</u>	

C3

	201		250
EG327	LNTGATTNVT NDNVTDDEKK RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
BZ198	LNTGATTNVT NDNVTDDEKK RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
BZ10	LNTGATTNVT NDNVTDDEKK RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
H15	LNTGATTNVT NDNVTDDEKK RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
EG329	LNTGATTNVT NDNVTDDEKK RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
PMC21	LNTGATTNVT NDNVTDDEKK RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
H38	LNTGATTNVT NDNVTDDEKK RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
P20	AGSSASHVDA GNQST..HYT RAASIKDVLN	AGWNIKGVT	GSTTGQSENV
Z2491	AGSSASHVDA GNQST..HYT RAASIKDVLN	AGWNIKGVT	GSTTGQSENV
H41	LNTGATTNVT NDNVTDDEKK RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
Consensus	<u>----A-----T-----</u>	<u>RAAS-KDVLN AGWNIKGVP- G-T-----NV</u>	

V3

C4

V4

	251		300
EG327	DFVRTYDTVE FLSADTKTTT VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
BZ198	DFVRTYDTVE FLSADTKTTT VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
BZ10	DFVRTYDTVE FLSADTKTTT VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
H15	DFVRTYDTVE FLSADTKTTT VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
EG329	DFVRTYDTVE FLSADTKTTT VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
PMC21	DFVRTYDTVE FLSADTKTTT VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
H38	DFVRTYDTVE FLSADTKTTT VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
P20	DFVRTYDTVE FLSADTKTTT VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
Z2491	DFVRTYDTVE FLSADTKTTT VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
H41	DFVRTYDTVE FLSADTKTTT VNVESKDNGK	KTEVKIGAKT	SVIKEKDGL
Consensus	<u>DFV-TYDTVE FLSADTKTTT VNVESKDNGK</u>	<u>-TEVKIGAKT SVIKEKDGL</u>	

C5

FIG. 1B



3/31

	301		350
EG327	VTGKDKGEND	SSTDKGEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGGQADK
BZ198	VTGKGKDENG	SSTDDEGEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGGQADK
BZ10	VTGKGKGENG	SSTDDEGEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGGQADK
H15	VTGKGKDENG	SSTDDEGEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGGQADK
EG329	VTGKDKGENG	SSTDDEGEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGGQADK
PMC21	VTGKDKGENG	SSTDDEGEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGGQADK
H38	VTGKGKGENG	SSTDDEGEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGGQADK
P20	VTGKGKGENG	SSTDDEGEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGGQADK
Z2491	VTGKGKGENG	SSTDDEGEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGGQADK
H41	VTGKGKGENG	SSTDDEGEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGGQADK
Consensus	<u>VTGK-K-EN-</u>	<u>SSTD-GEGLV</u>	<u>TAKEVIDAVN KAGWRMKT TT ANGQTGGQADK</u>

C5

	351		400
EG327	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
BZ198	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
BZ10	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
H15	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
EG329	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
PMC21	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
H38	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
P20	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
Z2491	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
H41	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
Consensus	<u>FETVTSGT-V</u>	<u>TFASG-GTTA</u>	<u>TVSKDDQGNI TV-YDVNVGD ALNVNQLQNS</u>

C5

	401		450
EG327	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
BZ198	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
BZ10	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
H15	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
EG329	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
PMC21	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
H38	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
P20	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
Z2491	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EISRNKGKNID
H41	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
Consensus	<u>GWNLDSKAVA</u>	<u>GSSGKVISGN</u>	<u>VSPSKGKMDE TVNINAGNNI EI-RNGKNID</u>

C5

FIG. 1C



4/31

	451	500
EG327	IATSMTPQFS SVSLGAGADA PTLSDVDEGA LNVGSKDANK	PVRITNVAPG
BZ198	IATSMAPQFS SVSLGAGADA PTLSDVDEGA LNVGSKDTNK	PVRITNVAPG
BZ10	IATSMTPQFS SVSLGAGADA PTLSDVDEGA LNVGSKDANK	PVRITNVAPG
H15	IATSMTPQFS SVSLGAGADA PTLSDVDEGA LNVGSKDANK	PVRITNVAPG
EG329	IATSMTPQFS SVSLGAGADA PTLSDVG.DA LNVGSKKDNK	PVRITNVAPG
PMC21	IATSMTPQFS SVSLGAGADA PTLSDVG.DA LNVGSKKDNK	PVRITNVAPG
H38	IATSMTPQFS SVSLGAGADA PTLSDVDDKA LNVGSKDANK	PVRITNVAPG
P20	IATSMTPQFS SVSLGAGADA PTLSDVDEGA LNVGSKDANK	PVRITNVAPG
Z2491	IATSMAPQFS SVSLGAGADA PTLSDVDEGA LNVGSKDANK	PVRITNVAPG
H41	IATSMTPQFS SVSLGAGADA PTLSDVDEGA LNVGSKDANK	PVRITNVAPG
Consensus	<u>IATSM-PQFS SVSLGAGADA PTLSDV---A LNVGSK--NK</u>	<u>PVRITNVAPG</u>

C5

	501	550
EG327	VKEGDVTNVA QLKGV AQNLN NHIDNVDGNA RAGIAQAIAT	AGLVQAYLPG
BZ198	VKEGDVTNVA QLKGV AQNLN NRIDNVDGNA RAGIAQAIAT	AGLVQAYLPG
BZ10	VKEGDVTNVA QLKGV AQNLN NRIDNVDGNA RAGIAQAIAT	AGLAQAYLPG
H15	VKEGDVTNVA QLKGV AQNLN NRIDNVDGNA RAGIAQAIAT	AGLAQAYLPG
EG329	VKEGDVTNVA QLKGV AQNLN NRIDNVDGNA RAGIAQAIAT	AGLVQAYLPG
PMC21	VKEGDVTNVA QLKGV AQNLN NRIDNVDGNA RAGIAQAIAT	AGLVQAYLPG
H38	VKEGDVTNVA QLKGV AQNLN NRIDNVDGNA RAGIAQAIAT	AGLVQAYLPG
P20	VKEGDVTNVA QLKGV AQNLN NRIDNVNGNA RAGIAQAIAT	AGLAQAYLPG
Z2491	VKEGDVTNVA QLKGV AQNLN NRIDNVDGNA RAGIAQAIAT	AGLVQAYLPG
H41	VKEGDVTNVA QLKGV AQNLN NRIDNVNGNA RAGIAQAIAT	AGLVQAYLPG
Consensus	<u>VKEGDVTNVA QLKGV AQNLN N-IDNV-GNA RAGIAQAIAT</u>	<u>AGL-QAYLPG</u>

C5

	551	600
EG327	KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS	RGHFGASASV
BZ198	KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS	RGHFGASASV
BZ10	KSMMAIGGGT YRGEAGYAIG YSSISDTGNW VIKGTASGNS	RGHFGTSASV
H15	KSMMAIGGGT YRGEAGYAIG YSSISDTGNW VIKGTASGNS	RGHFGASASV
EG329	KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS	RGHFGASASV
PMC21	KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS	RGHFGASASV
H38	KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS	RGHFGASASV
P20	KSMMAIGGGT YLGEAGYAIG YSSISDTGNW VIKGTASGNS	RGHFGTSASV
Z2491	KSMMAIGGGT YRGEAGYAIG YSSISDGGNW IIKGTASGNS	RGHFGASASV
H41	KSMMAIGGGT YLGEAGYAIG YSSISAGGNW IIKGTASGNS	RGHFGASASV
Consensus	<u>KSMMAIGG-T Y-GEAGYAIG YSSIS--GNW -IKGTASGNS</u>	<u>RGHFG-SASV</u>

C5

FIG. 1D



Title: Modified Surface Antigen
Inventor: Ian Richard Anselm Peak *et al.*
Appl. No.: 09/771,382 Customer No.: 570
Atty. Docket No.: 8795-24U1

5/31

	601
EG327	GYQW.
BZ198	GYQW.
BZ10	GYQW.
H15	GYQW.
EG329	GYQW.
PMC21	GYQW.
H38	GYQW.
P20	GYQW.
Z2491	GYQW.
H41	GYQW.
Consensus	<u>GYQW.</u>
	C5

FIG. 1E



6/31

```
1
H15 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCCTGGGT CGTCGTATCC GAGCTCACAC 70
BZ10 ATGAACAAAA TATCCCGCAT CATTGGAAT AGTGCCCTCA ATGCCTGGGT CGTCGTATCC GAGCTCACAC
BZ198 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCCTGGGT CGTCGTATCC GAGCTCACAC
P20 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCCTGGGT AGTCGTATCC GAGCTCACAC
H38 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
Z2491 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
H41 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
EG329 ATGAACGAAA TATTGCGCAT CATTGGAAT AGCGCCCTCA ATGCCTGGGT CGTTGTATCC GAGCTCACAC
PMC21 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCATGGGT CGTCGTATCC GAGCTCACAC
EG327 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCCTGGGT CGCCGTATCC GAGCTCACAC
Consensus ATGAAC-AAA TAT--CGCAT CATTGGAAT AG-GCCCTCA ATGC-TGGGT -G--GTATCC GAGCTCACAC
```

C1

```
71
H15 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACGTGTTGT TTGCAACGGT 140
BZ10 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACGTGTTGT TTGCAACGGT
BZ198 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACGTGTTGT TTGCAACGGT
P20 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACGTGTTGT CCGCAACGGT
H38 GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACACGTGTTGT TTGCAACGGT
Z2491 GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACACGTGTTGT TTGCAACGGT
H41 GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACACGTGTTGT TTGCAACGGT
EG329 GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT
PMC21 GCAACCACAC CAAACGCGCC TCCGCAACCG TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT
EG327 GCAACCACAC CAAACGCGCC TCCGCAACCG TGGCGACCGC CGTATTGGCG ACACGTGTTGT TTGCAACGGT
Consensus GCAACCACAC CAAACGCGCC TCCGCAACCG TG--GACCGC CGTATTGGCG AC-CTG-TGT --GCAACGGT
```

C1

```
141
H15 TCAGGCGAAT GCTACCGATG ACGAC..... GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC 210
BZ10 TCAGGCGAAT GCTACCGATG ACGAC..... GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
BZ198 TCAGGCGAAT GCTACCGATG ACGAC..... GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
P20 TCAGGCGAAT GCTACCGATA CCGAT..... GAAGATGAA GAGTTAGAAT CCGTAGCACG CTCTGCTCTG
H38 TCAGGCGAAT GCTACCGATG AAGAT..... GAAGAAGAA GAGTTAGAAT CCGTAGTACG CTCTGCTCTG
Z2491 TCAGGCGAAT GCTACCGATG AAGAT..... GAAGAAGAA GAGTTAGAAT CCGTACAACG CTCTGTCGTA
H41 TCAGGCGAAT GCTACCGATG AAGAT..... GAAGAAGAA GAGTTAGAAT CCGTACAACG CTCTG...TC
EG329 TCAGGCAAGT GCTAACAATG AAGAGCAAGA AGAAGATTTA TATTTAGACC CCGTGCTACG CACTGTTGCC
PMC21 TCAGGCAAGT GCTAACAATG AAGAGCAAGA AGAAGATTTA TATTTAGACC CCGTACAACG CACTGTTGCC
EG327 TCAGGCGAGT ACTACCGATG ACGAC..... GATTTA TATTTAGAAC CCGTACAACG CACTGCTGTC
Consensus TCAGGC-A-T -CTA-C-AT- --GA----- -GA---A -A-TTAGA-- CCGT---ACG C-CTG-----
```

C1

V1

FIG. 2A



7/31

211
H15 GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGGTAC AGAAGA...T TCAAATTGGG 280
BZ10 GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGGTAC AGAAGA...T TCAAATTGGG
BZ198 GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGGTAC AGAAGA...T TCAAATTGGG
P20 GTGTTGCAAT TCATGATCGA TAAAGAAGGC AATGGAGAAA TCGAATCTAC AGGAGA...T ATAGGTTGGA
H38 GTGTTGCAAT TCATGATCGA TAAAGAAGGC AATGGAGAAA ACGAATCTAC AGGAAA...T ATAGGTTGGA
Z2491 GGG...AGCAT TCAAG.CCAG TATGGAAGGC AGCGGCCAAT TGGAAACGAT ATCAT...T ATCAATGACT
H41 GTAGGGAGCA TTCAAGCCAG TATGGAAGGC AGCGTCAAT TGGAAACGAT A..... TCATTATCAA
EG329 GTGTTGATAG TCAATTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAAAAGT AGAAGAAAAT TCAGATTGGG
PMC21 GTGTTGATAG TCAATTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAAAAGT AGAAGAAAAT TCAGATTGGG
EG327 GTGTTGAGCT TCCGTTCCGA TAAAGAAGGC ACGGGAGAAA AAGAAGTTAC AGAAGA...T TCAAATTGGG
Consensus G-----T-----C--TA--GAAGGC A--G--GAA--GAA-----A-----

V1

281
H15 CAGTATATTT CGACGAGAAA AGAGTACTAA AAGCCGGAGC AATCACCCCTC AAAGCCGGCG ACAACCTGAA 350
BZ10 CAGTATATTT CGACGAGAAA AGAGTACTAA AAGCCGGAGC AATCACCCCTC AAAGCCGGCG ACAACCTGAA
BZ198 CAGTATATTT CGACGAGAAA AGAGTACTAA AAGCCGGAGC AATCACCCCTC AAAGCCGGCG ACAACCTGAA
P20 GTATATATTA CGACGATCAC AACACTCTAC ACGGCGCAAC CGTTACCCTC AAAGCCGGCG ACAACCTGAA
H38 GTATATATTA CGACAATCAC AACACTCTAC ACGGCGCAAC CGTTACCCTC AAAGCCGGCG ACAACCTGAA
Z2491 AACGACAGCA AGGAATTTGT AGACCCATAC ATAGTA....GTTACCCTC AAAGCCGGCG ACAACCTGAA
H41 TGACTAACGA CAGCAAGGAA TTTGTAGACC CATACTAGT AGTTACCCTC AAAGCCGGCG ACAACCTGAA
EG329 CAGTATATTT CAACGAGAAA GGAGTACTAA CAGCCAGAGA AATCACCCCTC AAAGCCGGCG ACAACCTGAA
PMC21 CAGTATATTT CAACGAGAAA GGAGTACTAA CAGCCAGAGA AATCACCCCTC AAAGCCGGCG ACAACCTGAA
EG327 GAGTATATTT CGACAAGAAA GGAGTACTAA CAGCCGGAAC AATCACCCCTC AAAGCCGGCG ACAACCTGAA
Consensus -----A-----T-ACCCTC AAAGCCGGCG ACAACCTGAA

V1

C2

351
H15 AATCAAACAA AACACCAATG AAAACACCAA TGAAAACACC AATGACAGTA GCTTCACCTA CTCCTGAAA 420
BZ10 AATCAAACAA AACACCAATG AAAACACCAA TGAAAACACC AATGACAGTA GCTTCACCTA CTCCTGAAA
BZ198 AATCAAACAA AACACCAATG AAAACACC...AATGACAGTA GCTTCACCTA CTCCTGAAA
P20 AATCAAACAA AGCGGCAAG A.....CTTCACCTA CTCGCTGAAA
H38 AATCAAACAA AACACCAATA AAAACACCAA TGAAAACACC AATGACAGTA GCTTCACCTA CTCGCTGAAA
Z2491 AATCAAACAA AACACCAATG AAAACACC...AATGCCAGTA GCTTCACCTA CTCGCTGAAA
H41 AATCAAACAA AACACCAATG AAAACACC...AATGCCAGTA GCTTCACCTA CTCGCTGAAA
EG329 AATCAAACAA AAC.....G.....GCACAA ACTTCACCTA CTCGCTGAAA
PMC21 AATCAAACAA AAC.....G.....GCACAA ACTTCACCTA CTCGCTGAAA
EG327 AATCAAACAA AACACCAATG AAAACACC...AATGCCAGTA GCTTCACCTA CTCGCTGAAA
Consensus AATCAAACAA A-C-----CTTCACCTA CTC-CTGAAA

C2

V2

C3

FIG. 2B



8/31

421 490
H15 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGT AATAAAGTCA
B210 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGT AATAAAGTCA
BZ198 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGT AATAAAGTCA
P20 AAAGAGCTGA AAGACCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGT AATAAAGTCA
H38 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGC AATAAAGTCA
Z2491 AAAGACCTCA CAGGCTGAT CAATGTTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGC AAGAAAGTCA
H41 AAAGACCTCA CAGGCTGAT CAATGTTGAA ACTGAAAAAT TATCGTTTGG CGCAAACGGC AAGAAAGTCA
EG329 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTTAG CGCAAACGGC AATAAAGTCA
PMC21 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTTAG CGCAAACGGC AATAAAGTCA
EG327 AAAGACCTCA CAGATCTGAC CAGTGTGAA ACTGAAAAAT TATCGTTTAG CGCAAACAGC AATAAAGTCA
Consensus AAAGA-CT-A -AG--CTGA- CA-TGTTG-A ACTGAAAAAT TATCGTTT-G CGCAAAC-G- AA-AAAGTCA

C3

491 560
H15 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
B210 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
BZ198 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
P20 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACCCCACGGT
H38 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
Z2491 ACATCATAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
H41 ACATCATAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
EG329 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
PMC21 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
EG327 ACATCACAAG CGACACCAAA GGCTTGAATT TTGCGAAAGA AACGGCTGAG ACCAACGGCG ACACCACGGT
Consensus ACATCA-AAG CGACACCAAA GGCTTGAATT T-GCGAAA-A AACGGCTG-G AC-AACGGCG AC-CCACGGT

C3

561 630
H15 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
B210 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
BZ198 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
P20 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTT GCGGGTTCTT CTGCTTCTCA CGTTGATGCG
H38 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
Z2491 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTT GCGGGTTCTT CTGCTTCTCA CGTTGATGCG
H41 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATATGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
EG329 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
PMC21 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
EG327 TCATCTGAAC GGTATCGGTT CGACTTTGAC CGATACGCTG CTGAATACCG GAGCGACCAC AAACGTAACC
Consensus TCATCTGAAC GGTAT-GGTT CGACTTTGAC CGATA-GCT- --G--T-C-- --GC--C--- ----G---C-

C3

V3

FIG. 2C



Title: Modified Surface Antigen
Inventor: Richard Anselm Peak *et al.*
Appln. #: 09/071,382 Customer No.: 570
Atty. Docket No.: 8795-24U1

9/31

```
631
H15 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGC GGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA 700
B210 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGC GGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
BZ198 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGC GGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
P20 GGTAAACCAA GTACACATTA C.....ACT CGTGC GGCAA GTATTAAAGGA TGTGTTGAAT GCGGGTTGGA
H38 AACGACAACG TTACCGATGA CAAGAAAAAA CGTGC GGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
Z2491 GGTAAACCAA GTACACATTA C.....ACT CGTGC GGCAA GTATTAAAGGA TGTGTTGAAT GCGGGTTGGA
H41 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGC GGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
EG329 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGC GGCAA GCGTTAAAGA CGTATTAAAC GCTGGCTGGA
PMC21 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGC GGCAA GCGTTAAAGA CGTATTAAAC GCTGGCTGGA
EG327 AACGACAACG TTACCGATGA CGAGAAAAAA CGTGC GGCAA GCGTTAAAGA CGTATTAAAC GCAGGCTGGA
Consensus -----AC-A-- -TAC--AT-A C-----A-- CGTGC-GCAA G--TTAA-GA -GT-TT-AA -GC-GG-TGGA
V3 C4
```

```
701
H15 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTTACGA 770
B210 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTC GATTTCGTCC GCACCTTACGA
BZ198 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTTACGA
P20 ATATTAAAGG TGTTAAACT GGTCAACAA CTGGTCAATC AGAAATGTC GATTTCGTCC GCACCTTACGA
H38 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC ACACCTTACGA
Z2491 ATATTAAAGG TGTTAAACT GGTCAACAA CTGGTCAATC AGAAATGTC GATTTCGTCC GCACCTTACGA
H41 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTTACGA
EG329 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTTACGA
PMC21 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTTACGA
EG327 ACATTAAAGG CGTTAAACCC GGTACAACAG CT.....TC CGATAACGTT GATTTCGTCC GCACCTTACGA
Consensus A-ATTAA-GG -GTTAA-C- GG--CAACA- CT-----TC -GA-AA-GT- GATTTCGTCC -CACTTACGA
C4 V4 C5
```

```
771
H15 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG 840
B210 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
BZ198 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
P20 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
H38 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
Z2491 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
H41 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
EG329 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
PMC21 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
EG327 CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
Consensus CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAAACGACT GTTAATGTGG AAAGCAAAGA CAACGGCAAG
C5
```

```
841
H15 AAAACCGAAG TTAATAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA 910
B210 AAAACCGAAG TTAATAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
BZ198 AAAACCGAAG TTAATAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
P20 AAAACCGAAG TTAATAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
H38 AAAACCGAAG TTAATAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
Z2491 AAAACCGAAG TTAATAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
H41 AAAACCGAAG TTAATAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
EG329 AAAACCGAAG TTAATAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
PMC21 AAAACCGAAG TTAATAATCGG TCGGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
EG327 AAAACCGAAG TTAATAATCGG TCGGAAGACT TCTGTTATCA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
Consensus A-AACCGAAG TTAATAATCGG TCGGAAGACT TCTGTTAT-A AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
C5
```

FIG. 2D



10/31

911 980
H15 AAGGCAAAGA CGAGAATGGT TCTTCTACAG ACGAAGGCCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
B210 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
B2198 AAGGCAAAGA CGAGAATGGT TCTTCTACAG ACGAAGGCCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
P20 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
H38 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
Z2491 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
H41 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
EG329 AAGACAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
PMC21 AAGACAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
EG327 AAGACAAAGG CGAGAATGAT TCTTCTACAG ACGAAGGCCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA
Consensus AAG-CAAAG- CGAGAATG-T TCTTCTACAG AC-AAGGCCGA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA

C5

981 1050
H15 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
B210 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
B2198 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
P20 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
H38 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
Z2491 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
H41 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
EG329 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
PMC21 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
EG327 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG
Consensus TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG

C5

1051 1120
H15 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACCTGCG ACTGTAAGTA
B210 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACCTGCG ACTGTAAGTA
B2198 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACCTGCG ACTGTAAGTA
P20 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACCTGCG ACTGTAAGTA
H38 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACCTGCG ACTGTAAGTA
Z2491 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACCTGCG ACTGTAAGTA
H41 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACCTGCG ACTGTAAGTA
EG329 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACCTGCG ACTGTAAGTA
PMC21 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACCTGCG ACTGTAAGTA
EG327 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACCTGCG ACTGTAAGTA
Consensus TTTGAAACCG TTACATCAGG CACAAA-GTA ACCTTTGCTA GTGGTAA-GG TACAACCTGCG ACTGTAAGTA

C5

1121 1190
H15 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
B210 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
B2198 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
P20 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
H38 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
Z2491 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
H41 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
EG329 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
PMC21 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
EG327 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT
Consensus AAGATGATCA AGGCAACATC ACTGTTA-GT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT

C5

FIG. 2E



11/31

1191 1260
H15 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTTCCTCGG GCAAAGTCAT CAGCGGCAAT
B210 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTTCCTCGG GCAAAGTCAT CAGCGGCAAT
B2198 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTTCCTCGG GCAAAGTCAT CAGCGGCAAT
P20 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTTCCTCGG GCAAAGTCAT CAGCGGCAAT
H38 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTTCCTCGG GCAAAGTCAT CAGCGGCAAT
Z2491 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTTCCTCGG GCAAAGTCAT CAGCGGCAAT
H41 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTTCCTCGG GCAAAGTCAT CAGCGGCAAT
EG329 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTTCCTCGG GCAAAGTCAT CAGCGGCAAT
PMC21 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTTCCTCGG GCAAAGTCAT CAGCGGCAAT
EG327 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTTCCTCGG GCAAAGTCAT CAGCGGCAAT
Consensus GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTTCCTCGG GCAAAGTCAT CAGCGGCAAT

C5

1261 1330
H15 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
B210 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
B2198 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
P20 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
H38 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
Z2491 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
H41 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
EG329 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
PMC21 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
EG327 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
Consensus GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC

C5

1331 1400
H15 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
B210 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
B2198 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
P20 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
H38 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
Z2491 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
H41 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
EG329 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
PMC21 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
EG327 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
Consensus GCAACGG-AA AAATATCGAC ATCGCCACTT CGATGACCCC GCA-TTTTCC AGCGTTTCGC TCGG-GCGGG

C5

1401 1470
H15 GCGGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
B210 GCGGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
B2198 GCGGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
P20 GCGGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
H38 GCGGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
Z2491 GCGAGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
H41 GCGGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
EG329 GCGGGATGCG CCCACTTTGA GCGTGGAT. . .GGGGACGCA TTGAATGTCG GCAGCAAGAA GGACAACAAA
PMC21 GCGGGATGCG CCCACTTTGA GCGTGGAT. . .GGGGACGCA TTGAATGTCG GCAGCAAGAA GGACAACAAA
EG327 GCGGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
Consensus GGC-GATGCG CCCACTTT-A GCGTGGAT-- ---GG-CGC- TTGAATGTCG GCAGCAAG-A ---CAACAAA

C5

FIG. 2F



12/31

```
1471
H15 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
B210 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
BZ198 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
P20 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
H38 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
Z2491 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
H41 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
EG329 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
PMC21 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
EG327 CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
Consensus CCCGTCCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG
```

C5

```
1541
H15 GTGTGGCGCA AAAC TTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
B210 GTGTGGCGCA AAAC TTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
BZ198 GCGTGGCGCA AAAC TTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
P20 GTGTGGCGCA AAAC TTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
H38 GCGTGGCGCA AAAC TTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
Z2491 GCGTGGCGCA AAAC TTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
H41 GTGTGGCGCA AAAC TTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
EG329 GCGTGGCGCA AAAC TTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
PMC21 GCGTGGCGCA AAAC TTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
EG327 GCGTGGCGCA AAAC TTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
Consensus G-GTGGCGCA AAAC TTGAAC AACCGCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC
```

C5

```
1611
H15 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
B210 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
BZ198 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
P20 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
H38 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
Z2491 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
H41 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
EG329 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
PMC21 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
EG327 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
Consensus GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTACT
```

C5

FIG. 2G



13/31

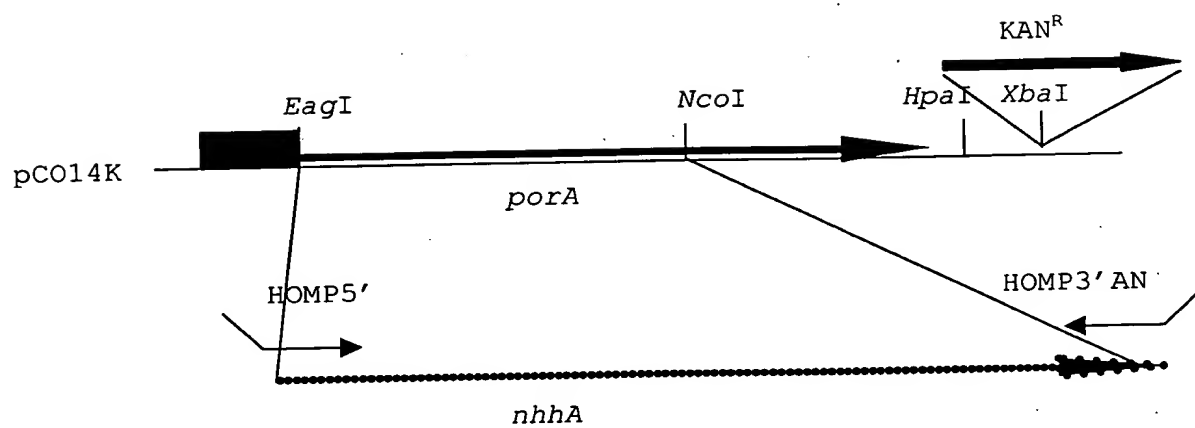
1681
H15 TATCGGGCGG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG 1750
B210 TATCGGGCGG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG
B2198 TATCGGGCGG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG
P20 TATCTCGGGG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG
H38 TATCGGGCGG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG
Z2491 TATCGGGCGG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG
H41 TATCTCGGGG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG
EG329 TATCGGGCGG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG
PMC21 TATCGGGCGG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG
EG327 TATCGGGCGG AAGCCGGTTA CGCCATCGGC TACTCGAGCA TTTCTGACAC TGGGAATTGG GTTATCAAGG
Consensus TATC-CGGCG AAGCCGGTTA -GCCATCGGC TACTC-AG-A TTTG-G-C-- -GG-AATTGG -TTATCAA-G

C5

1751
H15 GCACGGGCTTC CGGCAATTTC CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTATCAGT GGTAA 1815
B210 GCACGGGCTTC CGGCAATTTC CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTATCAGT GGTAA
B2198 GCACGGGCTTC CGGCAATTTC CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTATCAGT GGTAA
P20 GCACGGGCTTC CGGCAATTTC CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTATCAGT GGTAA
H38 GCACGGGCTTC CGGCAATTTC CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTATCAGT GGTAA
Z2491 GCACGGGCTTC CGGCAATTTC CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTATCAGT GGTAA
H41 GCACGGGCTTC CGGCAATTTC CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTATCAGT GGTAA
EG329 GCACGGGCTTC CGGCAATTTC CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTATCAGT GGTAA
PMC21 GCACGGGCTTC CGGCAATTTC CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTATCAGT GGTAA
EG327 GCACGGGCTTC CGGCAATTTC CGCGGCCATT TCGGTGCTTC CGCATCTGTC GGTATCAGT GGTAA
Consensus GCACGGGCTTC CGGCAATTTC CGCGGCCATT TCGGT-CCTC CGCATCTGTC GGTATCA-T GGTAA

C5

FIG. 2H

**FIG. 3A**

PIP52 (PMC21)

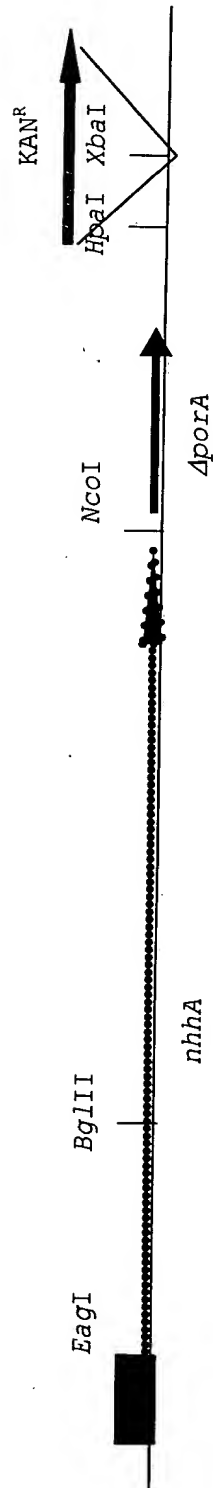


FIG. 3B

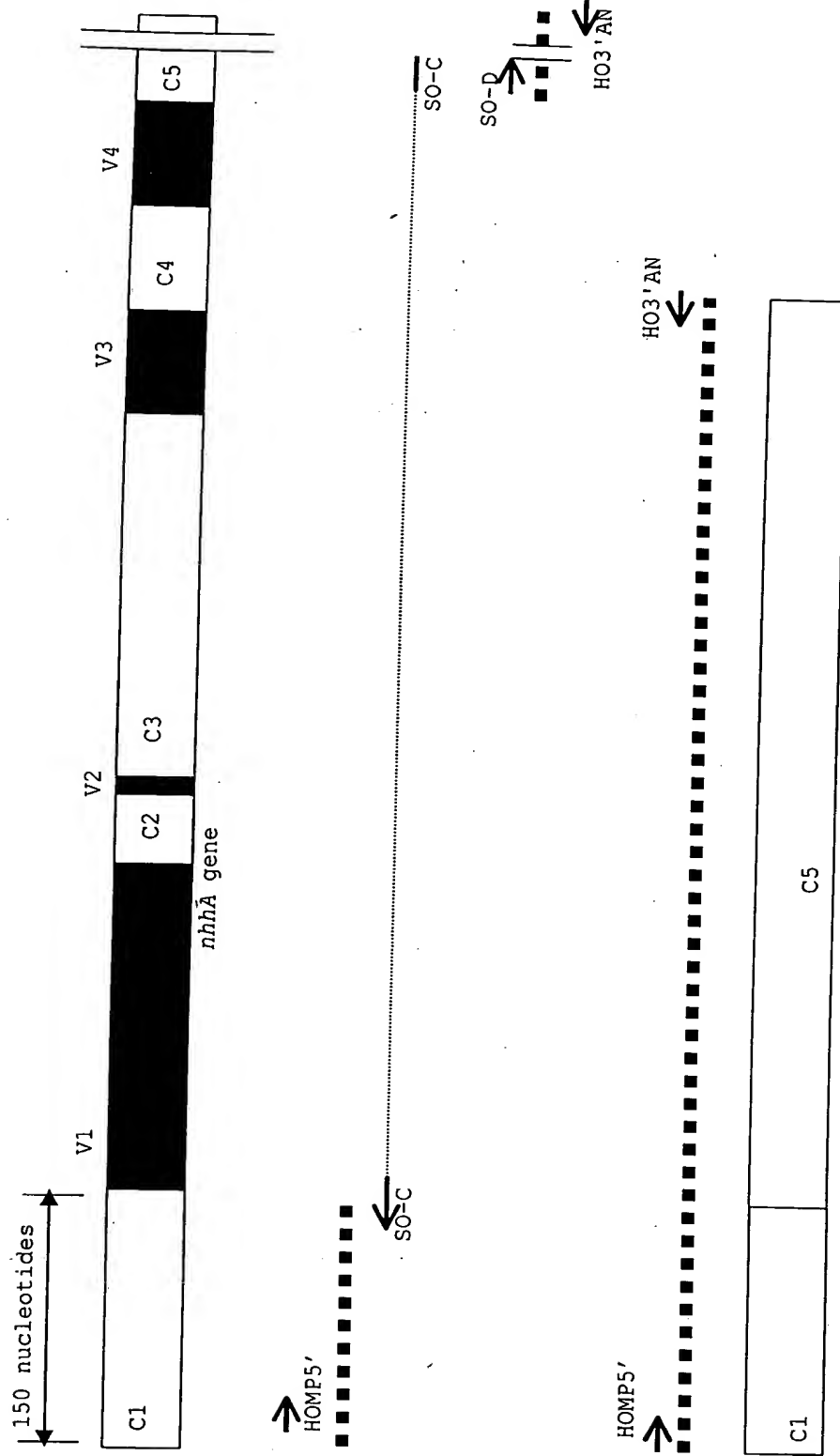


FIG. 4A

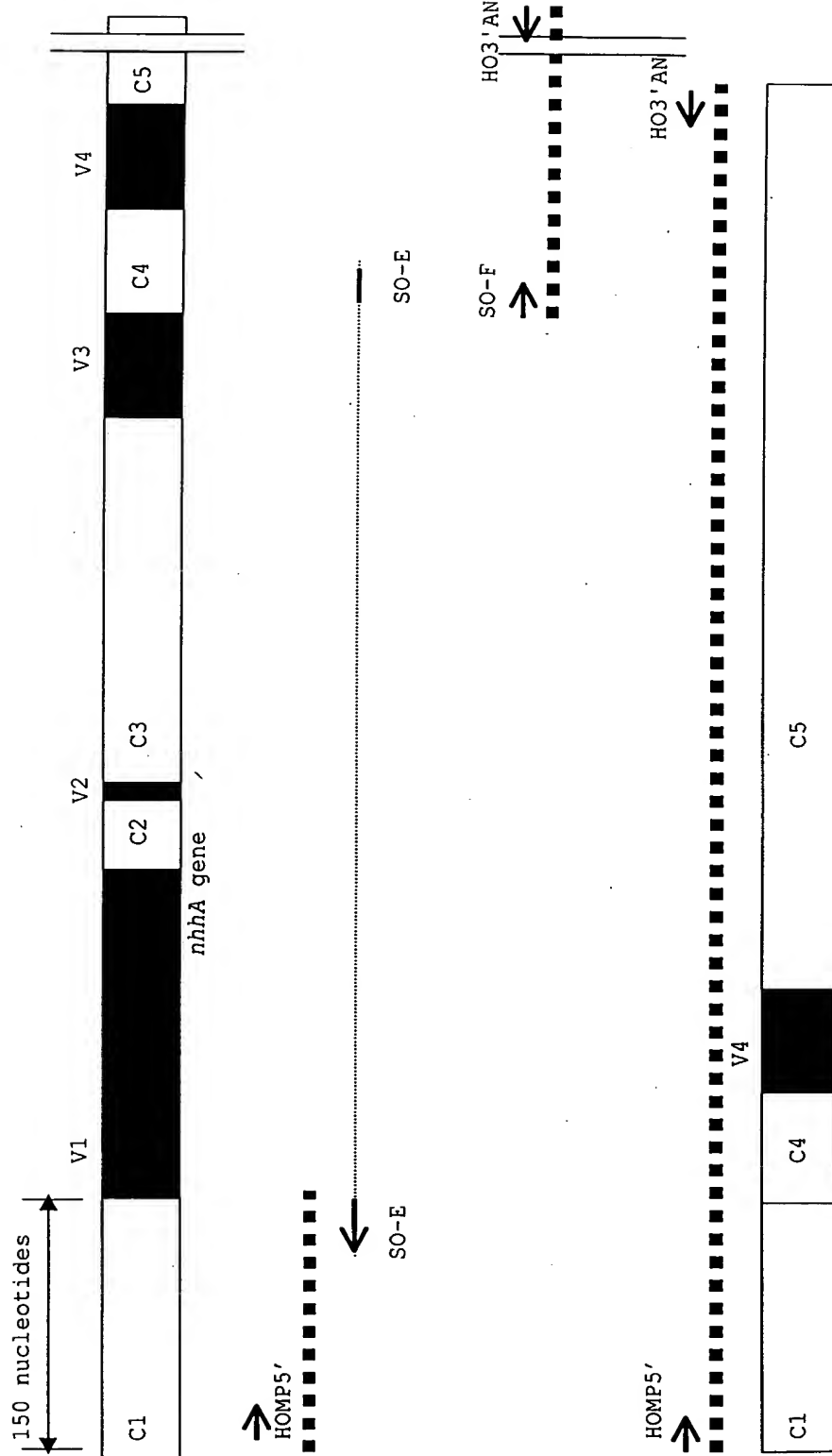


FIG. 4B

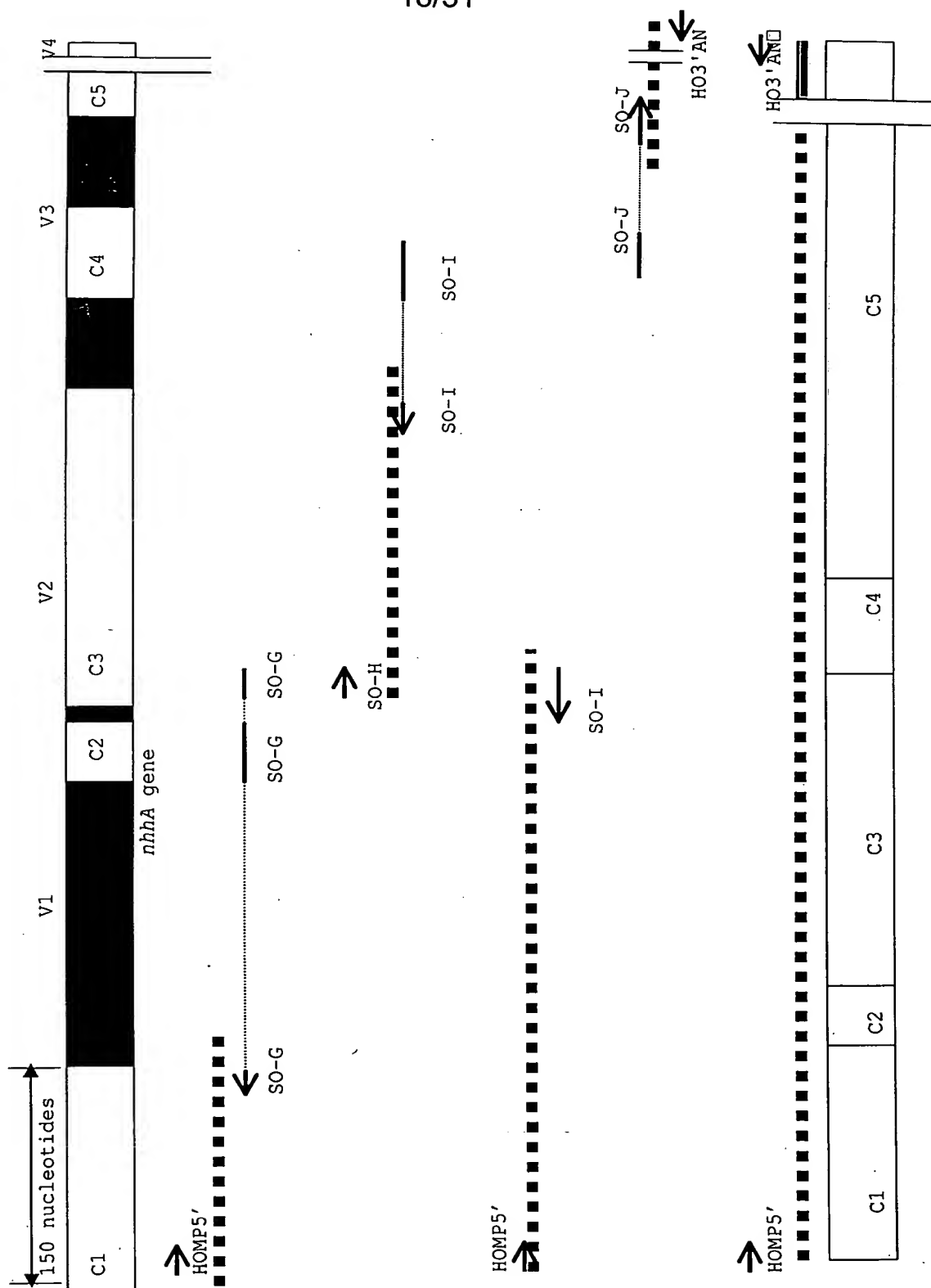


FIG. 4C

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANNETDLTSV GTEKLSFSAN GNKNVITS DT KGLNFAKETA GTNGDTTVHL
 101 NGIGSTLTDT LLNTGATTNV TNDNVTDDEK KRAASVKDVL NAGWNIKGVK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
 201 VIKKDKGLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
 251 NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA
 301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV
 401 RITNVAPGVK EGDVTNVAQL KGVAQNLNNR IDNV DGNARA GIAQAIATAG
 451 LVQAYLPKGS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG
 501 HFGASASVGY QW*

FIG. 5A

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACAATG AAACAGATCT GACCAGTGTT GGAAGTGAAG AATTATCGTT
 201 TAGCGCAAAC GGCAATAAAG TCAACATCAC AAGCGACACC AAAGGCTTGA
 251 ATTTTGCGAA AGAAACGGCT GGGACGAACG GCGACACCAC GGTTCATCTG
 301 AACGGTATTG GTTCGACTTT GACCGATACG CTGCTGAATA CCGGAGCGAC
 351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG
 401 CAAGCGTTAA AGACGTATTA AACGCTGGCT GGAACATTAA AGGCGTTAAA
 451 CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCCGCA CTTACGACAC
 501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGAAG
 551 GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT
 601 GTTATTAAAG AAAAAGACGG TAAGTTGGTT ACTGGTAAAG ACAAAGGCGA
 651 GAATGGTTCT TCTACAGACG AAGGCGAAGG CTTAGTGAAG GCAAAGGAAG
 701 TGATTGATGC AGTAAACAAG GCTGGTTGGA GAATGAAAAC AACACCGCT
 751 AATGGTCAAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC
 801 AAATGTAACC TTTGCTAGTG GTAAAGGTAC AACTGCGACT GTAAGTAAAG
 851 ATGATCAAGG CAACATCACT GTTATGTATG ATGTAAATGT CGGCGATGCC
 901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAATTTGG ATTCCAAAGC
 951 GGTTGCAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA
 1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG
 1051 ATTACCCGCA ACGGTAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA
 1101 GTTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTGAGCG
 1151 TGGATGGGGA CGCATTGAAT GTCGGCAGCA AGAAGGACAA CAAACCCGTC
 1201 CGCATTACCA ATGTCGCCCC GGGCGTTAAA GAGGGGGATG TTACAAACGT
 1251 CGCACAACTT AAAGGCGTGG CGCAAACTT GAACAACCGC ATCGACAATG
 1301 TGGACGGCAA CGCGCGTGCG GGCATCGCCC AAGCGATTGC AACCGCAGGT
 1351 CTGGTTCAGG CGTATTTGCC CGGCAAGAGT ATGATGGCGA TCGGCGGCGG
 1401 CACTTATCGC GGCGAAGCCG GTTACGCCAT CGGCTACTCC AGTATTTCCG
 1451 ACGGCGGAAA TTGGATTATC AAAGGCACGG CTTCCGGCAA TTCGCGCGGC
 1501 CATTTCCGGT GCTTCCGCATC TGTCGGTTAT CAGTGGTAA

FIG. 5B

```

1  MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN
51  ATDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDTTVHL
101 NGIGSTLTDM LLNTGATTNV TNDNVTDEK KRAASVKDVL NAGWNIKGVK
151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
201 VIKEDGKLV TGKKGGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTSTA
251 NGQTGQADKF ETVTSGTKVT FASNGTTAT VSKDDQGNIT VKYDVNVGDA
301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE
351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP
401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA
451 GLVQAYLPK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR
501 GHFGASASVG YQW*

```

FIG. 6A

```

1  ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGGGT
51  CGCCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
101 TGAAGACCGC CGTATTGGCG ACACGTGTGT TTGCAACGGT TCAGGCGAAT
151 GCTACCGATG AAACAGGCCT GATCAATGTT GAAACTGAAA AATTATCGTT
201 TGGCGCAAAC GGCAAGAAAG TCAACATCAT AAGCGACACC AAAGGCTTGA
251 ATTTTCGCGAA AGAAACGGCT GGGACGAACG GCGACACCAC GGTTCATCTG
301 AACGGTATCG GTTCGACTTT GACCGATATG CTGCTGAATA CCGGAGCGAC
351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG
401 CAAGCGTTAA AGACGTATTA AACGCAGGCT GGAACATTAA AGGCGTTAAA
451 CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCCGCA CTTACGACAC
501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACCGACTGT AATGTGGAAA
551 GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT
601 GTTATTAAAG AAAAAGACGG TAAGTTGGTT ACTGGTAAAG GCAAAGGCGA
651 GAATGGTTCT TCTACAGACG AAGGCGAAGG CTTAGTGACT GCAAAAAGAA
701 TGATTGATGC AGTAAACAAG GCTGGTTGGA GAATGAAAAC AACAAACGCT
751 AATGGTCAAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC
801 AAAAGTAACC TTTGCTAGTG GTAATGGTAC AACTGCGACT GTAAGTAAAG
851 ATGATCAAGG CAACATCACT GTTAAGTATG ATGTAAATGT CGGCGATGCC
901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAAATTTGG ATTCCAAAGC
951 GGTTGCAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA
1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG
1051 ATTACCCGCA ACGGCAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA
1101 ATTTTCCAGC GTTTCGCTCG GCGCGGGGCG GGATGCGCCC ACTTTAAGCG
1151 TGGATGACGA GGGCGCGTTG AATGTCGGCA GCAAGGATGC CAACAAACCC
1201 GTCCGCATTA CCAATGTCGC CCCGGGCGTT AAAGAGGGGG ATGTTACAAA
1251 CGTCGCGCAA CTTAAAGGTG TGGCGCAAAA CTTGAACAAC CGCATCGACA
1301 ATGTGAACGG CAACGCGCGT GCGGGCATCG CCCAAGCGAT TGCAACCGCA
1351 GGTCTGGTTC AGGCGTATCT GCCCGCAAG AGTATGATGG CGATCGGCGG
1401 CGGCACTTAT CTCGGCGAAG CCGGTTATGC CATCGGCTAC TCAAGCATTT
1451 CCGCCGGCGG AAATTGGATT ATCAAAGGCA CGGCTTCCGG CAATTGCGCG
1501 GGCCATTTTC GTGCTTCCGC ATCTGTCGGT TATCAGTGGT AA

```

FIG. 6B

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANNVDVVRTY DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK
 101 DGKLVTKGDK GENGSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG
 151 QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ
 201 LQNSGWNLDS KAVAGSSGKV ISGNVSPSKG KMDETVNINA GNNIEITRNG
 251 KNIDIATSMT PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVIRITNV
 301 APGVKEGDVT NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY
 351 LPGKSMMMAIG GGTyrGEAGY AIGYSSISDG GNWIIKGTAS GNSRGHFGAS
 401 ASVGyQW*

FIG. 7A

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACAAACG TTGATTTTCGT CCGCACTTAC GACACAGTCG AGTTCCTTGAG
 201 CGCAGATACG AAAACAACGA CTGTTAATGT GGAAAGCAAA GACAACGGCA
 251 AGAAAAACCGA AGTTAAAATC GGTGCGAAGA CTTCTGTTAT TAAAGAAAAA
 301 GACGGTAAGT TGGTTACTGG TAAAGACAAA GGCGAGAATG GTTCTTCTAC
 351 AGACGAAGGC GAAGGCTTAG TGAAGTGAAG AGAAGTGATT GATGCAGTAA
 401 ACAAGGCTGG TTGGAGAATG AAAACAACAA CCGCTAATGG TCAAACAGGT
 451 CAAGCTGACA AGTTTGAAAC CGTTACATCA GGCACAAATG TAACCTTTGC
 501 TAGTGGTAAA GGTACAACCTG CGACTGTAAG TAAAGATGAT CAAGGCAACA
 551 TCACTGTTAT GTATGATGTA AATGTCGGCG ATGCCCTAAA CGTCAATCAG
 601 CTGCAAAACA GCGGTTGGAA TTTGGATTCC AAAGCGGTTG CAGGTTCTTC
 651 GGGCAAAGTC ATCAGCGGCA ATGTTTCGCC GAGCAAGGGA AAGATGGATG
 701 AAACCGTCAA CATTAATGCC GGCAACAACA TCGAGATTAC CCGCAACGGT
 751 AAAAATATCG ACATCGCCAC TTCGATGACC CCGCAGTTTT CCAGCGTTTC
 801 GCTCGGCGCG GGGGCGGATG CGCCCACTTT GAGCGTGGAT GGGGACGCAT
 851 TGAATGTCGG CAGCAAGAAG GACAACAAAC CCGTCCGCAT TACCAATGTC
 901 GCCCCGGGCG TTAAAGAGGG GGATGTTACA AACGTCGCAC AACTTAAAGG
 951 CGTGGCGCAA AACTTGAACA ACCGCATCGA CAATGTGGAC GGCAACGCGC
 1001 GTGCGGGCAT CGCCCAAGCG ATTGCAACCG CAGGTCTGGT TCAGGCGTAT
 1051 TTGCCCCGCA AGAGTATGAT GCGGATCGGC GCGGCGACTT ATCGCGGCGA
 1101 AGCCGGTTAC GCCATCGGCT ACTCCAGTAT TTCCGACGGC GGAAATTGGA
 1151 TTATCAAAGG CACGGCTTCC GGCAATTCGC GCGGCCATTT CCGTGCTTCC
 1201 GCATCTGTCTG GTTATCAGTG GTAA

FIG. 7B

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT
 101 VNVESKDNGK KTEVKIGAKT SVIKEKDGKL VTGKDKGENG SSTDEGEGLV
 151 TAKEVIDAVN KAGWRMKTIT ANGQTGQADK FETVTSGTNV TFASGKGTTA
 201 TVSKDDQONI TVMYDVNVGD ALNVNQLQNS GWNLDSKAVA GSSGKVISGN
 251 VSPSKGKMDE TVNINAGNNI EITRNGKNID IATSMTPQFS SVSLGAGADA
 301 PTLSDGDAL NVGSKKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN
 351 RIDNVDGNAR AGIAQAIATA GLVQAYLPK SMMAIGGGTY RGEAGYAIGY
 401 SSISDGGNWI IKGTASGNSR GHFGASASVG YQW*

FIG. 8A

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACCGTG CGGCAAGCGT TAAAGACGTA TTAAACGCTG GCTGGAACAT
 201 TAAAGGCGTT AAACCCGCTA CAACAGCTTC CGATAACGTT GATTTCGTCC
 251 GCACTTACGA CACAGTCGAG TTCTTGAGCG CAGATACGAA AACAACTACT
 301 GTTAATGTGG AAAGCAAAGA CAACGGCAAG AAAACCGAAG TTAAATGCTA
 351 TCGCAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 401 AAGACAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCGA AGGCTTAGTG
 451 ACTGCAAAAG AAGTGATTGA TGCAGTAAAC AAGGCTGGTT GGAGAATGAA
 501 AACAAACACC GCTAATGGTC AAACAGGTCA AGCTGACAAG TTTGAAACCG
 551 TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAAAGG TACAACGCG
 601 ACTGTAAGTA AAGATGATCA AGGCAACATC ACTGTTATGT ATGATGTAAA
 651 TGTCGGCGAT GCCCTAAACG TCAATCAGCT GCAAAACAGC GGTGGAATT
 701 TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT
 751 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG
 801 CAACAACATC GAGATTACCC GCAACGGTAA AAATATCGAC ATCGCCACTT
 851 CGATGACCCC GCAGTTTTCC AGCGTTTCGC TCGGCGCGGG GCGGATGCG
 901 CCCACTTTGA GCGTGGATGG GGACGCATTG AATGTCGGCA GCAAGAAGGA
 951 CAACAAACCC GTCCGCATTA CCAATGTCGC CCCGGGCGTT AAAGAGGGGG
 1001 ATGTTACAAA CGTCGCACAA CTTAAAGGCG TGGCGCAAAA CTTGAACAAC
 1051 CGCATCGACA ATGTGGACGG CAACGCGCGT GCGGGCATCG CCCAAGCGAT
 1101 TGCAACCGCA GGTCTGGTTC AGCGGTATTT GCCCGGCAAG AGTATGATGG
 1151 CGATCGGCGG CGGCACTTAT CGCGGCGAAG CCGGTTACGC CATCGGCTAC
 1201 TCCAGTATTT CCGACGGCGG AAATTGGATT ATCAAAGGCA CGGCTTCCGG
 1251 CAATTCGCGC GGCCATTTCC GTGCTCCGC ATCTGTCGGT TATCAGTGGT
 1301 AA

FIG. 8B

```

1  MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
51 ANTLKAGDNL KIKQFTYSLK KDLDLTSVG TEKLSFSANG NKNVITSDTK
101 GLNFAKETAG TNGDTTVHLN GIGSTLTDRASV KDV LNAG WNIKG VKNVD
151 FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS VIKEDGKLV
201 TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA NGQTGQADKF
251 ETVTSGTNTV FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG
301 WNLDKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE ITRNGKNIDI
351 ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK
401 EGDVTNVAQL KGVAQN LNNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS
451 MMAIGGGTYR GEAGYAIGYS SISDGGNWII KG TASGNSRG HFGASASVGY
501 QW*

```

FIG. 9A

```

1  ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT
51  CGTCGTATCC GAGCTCACAC GCAACCGCAC CAAACGCGCC TCCGCAACCG
101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
151 GCTAACACCC TCAAAGCCGG CGACAACCTG AAAATCAAAC AATTCACCTA
201 CTCGCTGAAA AAAGACCTCA CAGATCTGAC CAGTGTTGGA ACTGAAAAAT
251 TATCGTTTAG CGCAAACGGC AATAAAGTCA ACATCACAAG CGACACCAAA
301 GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGGCG ACACCACGGT
351 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATCGTGCG GCAAGCGTTA
401 AAGACGTATT AAACGCTGGC TGGAACATTA AAGGCGTTAA AAACGTTGAT
451 TTCGTCCGCA CTTACGACAC AGTCGAGTTC TTGAGCGCAG ATACGAAAAC
501 AACGACTGTT AATGTGGAAA GCAAAGACAA CGGCAAGAAA ACCGAAGTTA
551 AAATCGGTGC GAAGACTTCT GTTATTAAAG AAAAAGACGG TAAGTTGGTT
601 ACTGGTAAAG ACAAAGGCGA GAATGGTTCT TCTACAGACG AAGGCGAAGG
651 CTTAGTGACT GCAAAGAAG TGATTGATGC AGTAAACAAG GCTGGTTGGA
701 GAATGAAAAC AACAACCGCT AATGGTCAAA CAGGTCAAGC TGACAAGTTT
751 GAAACCGTTA CATCAGGCAC AAATGTAACC TTTGCTAGTG GTAAAGGTAC
801 AACTGCGACT GTAAGTAAAG ATGATCAAGG CAACATCACT GTTATGTATG
851 ATGTAAATGT CGGCGATGCC CTAAACGTCA ATCAGCTGCA AAACAGCGGT
901 TGGAATTTGG ATTCCAAAGC GGTTCGAGGT TCTTCGGGCA AAGTCATCAG
951 CGGCAATGTT TCGCCGAGCA AGGGAAAGAT GGATGAAACC GTCAACATTA
1001 ATGCCGGCAA CAACATCGAG ATTACCCGCA ACGGTAAAAA TATCGACATC
1051 GCCACTTCGA TGACCCCGCA GTTTTCCAGC GTTTCGCTCG GCGCGGGGGC
1101 GGATGCGCCC ACTTTGAGCG TGGATGGGGA CGCATTGAAT GTCGGCAGCA
1151 AGAAGGACAA CAAACCCGTC CGCATTACCA ATGTCGCCCC GGGCGTTAAA
1201 GAGGGGGATG TTACAAACGT CGCACAACTT AAAGGCGTGG CGCAAACTT
1251 GAACAACCGC ATCGACAATG TGGACGGCAA CGCGCGTGCG GGCATCGCCC
1301 AAGCGATTGC AACCAGAGT CTGGTTCAGG CGTATTTGCC CGGCAAGAGT
1351 ATGATGGCGA TCGGCGGCGG CACTTATCGC GGCGAAGCCG GTTACGCCAT
1401 CGGCTACTCC AGTATTTCCG ACGGCGGAAA TTGGATTATC AAAGGCACGG
1451 CTTCCGGCAA TTCGCGCGGC CATTTCCGGT CTTCCGCATC TGTCGGTTAT
1501 CAGTGGTAA

```

FIG. 9B



24/31

1 50
H41 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN
PMC21 MNKIYRIIWN SALNAWVVVS DLTRNHTKRA SATVNTAVLA TLLFATVOAS
H41Studel MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN
PMC21Bgldel MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVOAS
PMC21C1C5 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVOAS
C1

51 100
H41 ATDED...EEE ELESVQRS.V VGSIQASMEG SVELET...I SLSMTNDSKE
PMC21 ANNEEQEEYL YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK
H41Studel ATDE.....
PMC21Bgldel ANNE.....
PMC21C1C5 AN.....
V1

101 150
H41 FVDPYIVVTL KAGDNLKIKO N.TNENTNAS SFTYSLKKDL TGLINVETEK
PMC21 GVLTAAREITL KAGDNLKIKO NGTN.....FTYSLKKDL TDLTSVGTEK
H41Studel TGLINVETEK
PMC21Bgldel TDLTSVGTEK
PMC21C1C5
V1 C2 V2 C3

151 200
H41 LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT
PMC21 LSFSAHGKVV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDTLLNT
H41Studel LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT
PMC21Bgldel LSFSANGKVV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDTLLNT
PMC21C1C5
C3 V3

201 250
H41 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT
PMC21 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT
H41Studel GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT
PMC21Bgldel GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT
PMC21C1C5NVDFVRT
V3 C4 V4 C5

251 300
H41 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTKGK
PMC21 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTKGD
H41Studel YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTKGK
PMC21Bgldel YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTKGD
PMC21C1C5 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTKGD
C5

301 350
H41 KGEGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
PMC21 KGEGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
H41Studel KGEGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
PMC21Bgldel KGEGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
PMC21C1C5 KGEGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT
C5

351 400
H41 SGTKVTFASG NGTTATVSKD DOGNITVKYD VNVGDALNVN QLQNSGWNLD
PMC21 SGTNVTFASG KGTATVSKD DOGNITVMYD VNVGDALNVN QLQNSGWNLD
H41Studel SGTKVTFASG NGTTATVSKD DOGNITVKYD VNVGDALNVN QLQNSGWNLD
PMC21Bgldel SGTNVTFASG KGTATVSKD DOGNITVMYD VNVGDALNVN QLQNSGWNLD
PMC21C1C5 SGTNVTFASG KGTATVSKD DOGNITVMYD VNVGDALNVN QLQNSGWNLD
C5

FIG. 10A



25/31

401 450
H41 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
H41Studel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21Bgldel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21C1C5 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
C5

451 500
H41 TPOFSSVSLG AGADAPTLV DDEGALNVGS KDANKPVVIT NVAPGVKEGD
PMC21 TPOFSSVSLG AGADAPTLV DG.DALNVGS KKDANKPVVIT NVAPGVKEGD
H41Studel TPOFSSVSLG AGADAPTLV DDEGALNVGS KDANKPVVIT NVAPGVKEGD
PMC21Bgldel TPOFSSVSLG AGADAPTLV DG.DALNVGS KKDANKPVVIT NVAPGVKEGD
PMC21C1C5 TPOFSSVSLG AGADAPTLV DG.DALNVGS KKDANKPVVIT NVAPGVKEGD
C5

501 550
H41 VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMMA
PMC21 VTNVAQLKGV AQNLNNRIDN VDG NARAGIA QAIATAGLVQ AYLPGKSMMMA
H41Studel VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMMA
PMC21Bgldel VTNVAQLKGV AQNLNNRIDN VDG NARAGIA QAIATAGLVQ AYLPGKSMMMA
PMC21C1C5 VTNVAQLKGV AQNLNNRIDN VDG NARAGIA QAIATAGLVQ AYLPGKSMMMA
C5

551 600
H41 IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.
PMC21 IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
H41Studel IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.
PMC21Bgldel IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
PMC21C1C5 IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
C5

FIG. 10B

1 2 3 4 5 6

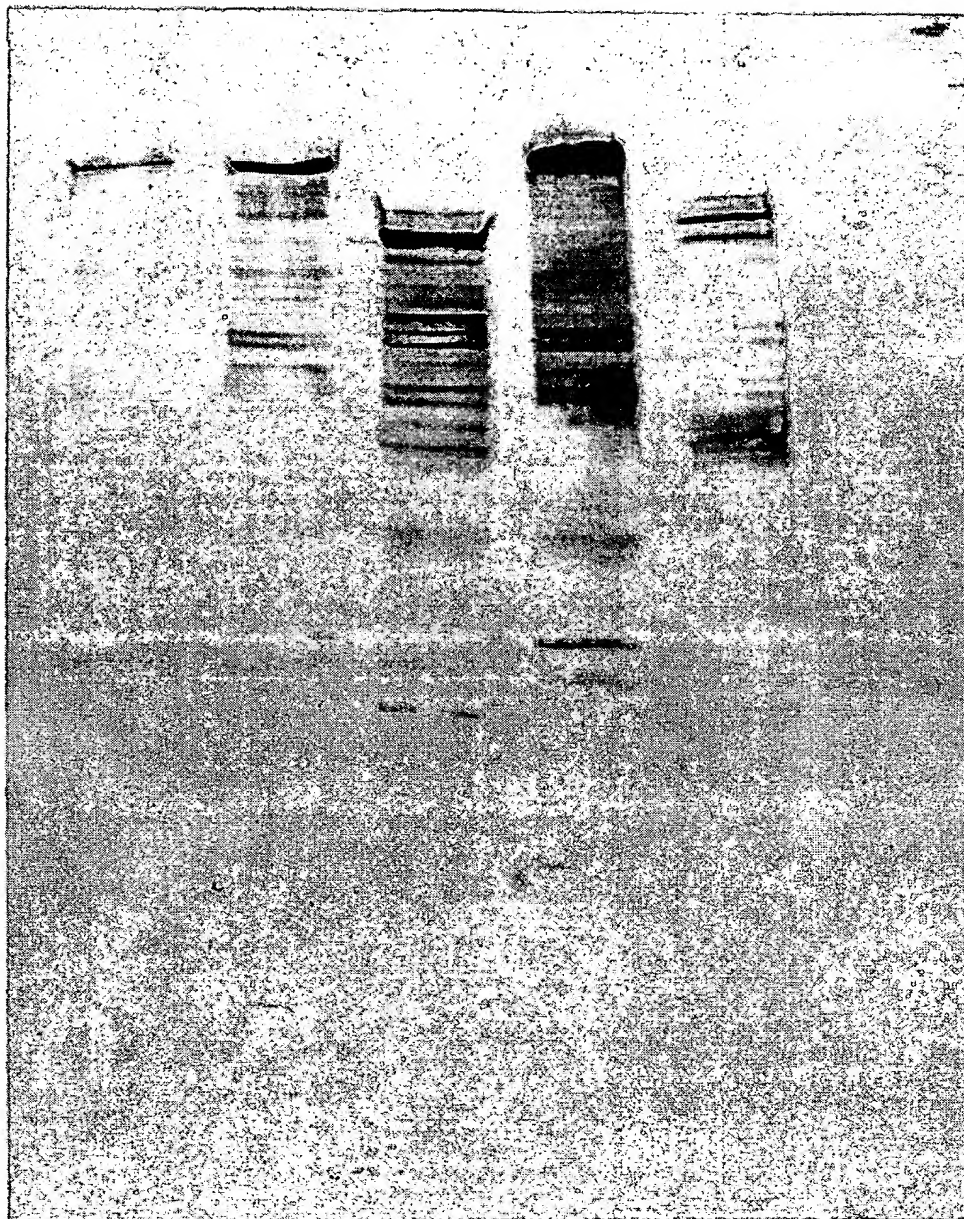


FIG. 11

1 2 3 4 5 6 7

09771382.071301

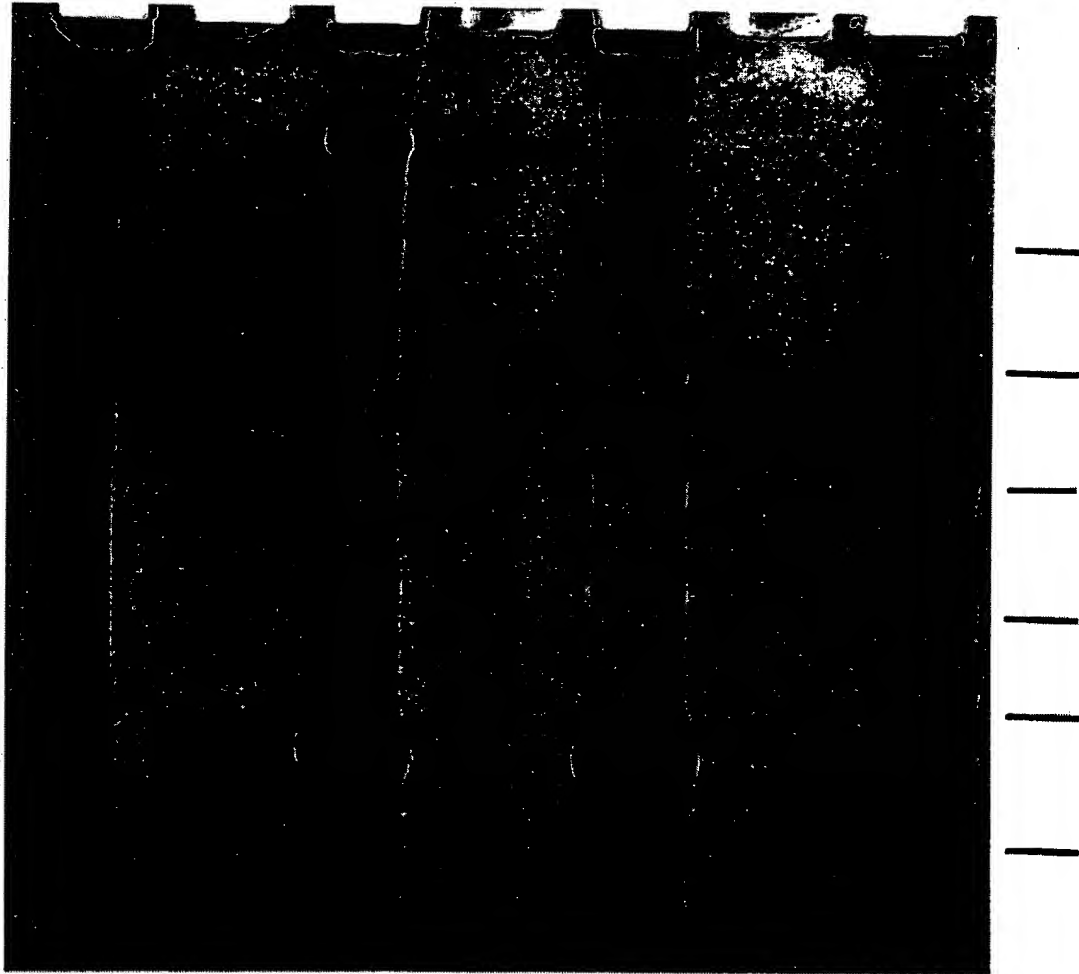
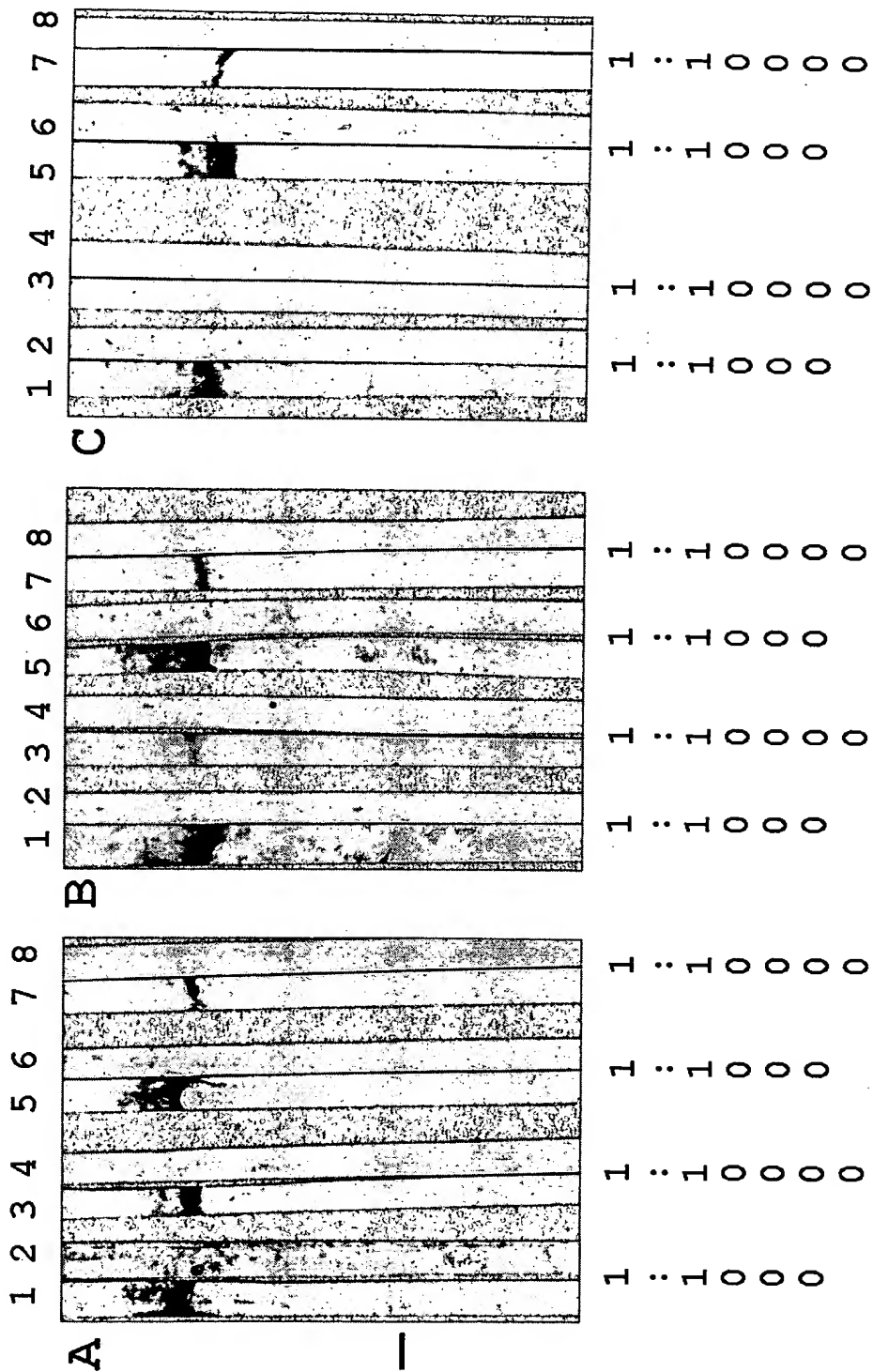


FIG. 12



173—

FIG. 13

52 NNEEQEEYL YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK
 101 GVLTAAREITL KAGDNLKIKQ NGTNFTYSLK KDLTDLTSVG TEKLSFSAHG
 151 NKVNITS DTK GLNFAKETAG TNGDITVHLN GIGSTLTDTL LNTGATTNVT
 201 NDNVTDDEKK RAASVKDVLN AGWNIKGVPK GTTASDNVDF VRTYDTVEFL
 251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGLVT GKDKGENGSS
 301 TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTNVTF
 351 ASGKGTTATV SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
 401 SGKVISGNVS PSKGKMDTV NINAGNNIEI TRNGKNIDIA TSMT PQFSSV
 451 SLGAGADAPT LSVGDALNV GSKKDNKPVR ITNVAPGVKE GDVTNVAQLK
 501 GVAQNLNNRI DNVDGNARAG IAQAIATAGL VQAYLPGKSM MAIGGGTYRG
 551 EAGYAIGYSS ISDGGNWIIG GTASGNSRGH FGASASVG YQ W*

FIG. 14A

52 TDEDEEEEL ESVQRSVVG S IQASMEGSVE LETISLSMTN DSKEFVDPYI
 101 VVTLKAGDNL KIKQNTNENT NASSFTYSLK KDLTG LINVE TEKLSFGANG
 151 KKVNIISDTK GLNFAKETAG TNGDITVHLN GIGSTLT DML LNTGATTNVT
 201 NDNVTDDEKK RAASVKDVLN AGWNIKGVPK GTTASDNVDF VRTYDTVEFL
 251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGLVT GKDKGENGSS
 301 TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTKVTF
 351 ASGNGTTATV SKDDQGNITV KYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
 401 SGKVISGNVS PSKGKMDTV NINAGNNIEI TRNGKNIDIA TSMT PQFSSV
 451 SLGAGADAPT LSVDDGALN VGSKDANKPV RITNVAPGVK EGDVTNVAQL
 501 KGVAQNLNNR IDNVNGNARA GIAQAIATAG LVQAYLPGKS MMAIGGGTYL
 551 GEAGYAIGYS SISAGGNWII KGTASGNSRG HFGASASVG Y QW*

FIG. 14B

52 NNETDLTSV GTEKLSFSAN GNKVNITS DT KGLNFAKETA GTNGD TTVHL
 101 NGIGSTLTDT LLNTGATTNV TNDNVTDDEK KRAASVKDVL NAGWNIKG VK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
 201 VIKEDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
 251 NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA
 301 LNVNQLQNSG WNLD SKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV
 401 RITNVAPGVK EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG
 451 LVQAYLP GKS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG
 501 HFGASASVGY QW*

FIG. 14C

52 TDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGD TTVHL
 101 NGIGSTLTDM LLNTGATTNV TNDNVTDDEK KRAASVKDVL NAGWNIKG VK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
 201 VIKEDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
 251 NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA
 301 LNVNQLQNSG WNLD SKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP
 401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA
 451 GLVQAYLP GK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR
 501 GHFGASASVG YQW*

FIG. 14D

52 NNVDFVRTY DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK
 101 DGKLVTKGDK GENGSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG
 151 QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ
 201 LQNSGWNLDS KAVAGSSGKV ISGNVSPSKG KMDETVNINA GNNIEITRNG
 251 KNIDIATSMT PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVTRITNV
 301 APGVKEGDVT NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY
 351 LPGKSMMAIG GGTyrGEAGY AIGYSSISDG GNWIIKGTAS GNSRGHFGAS
 401 ASVGyQW*

FIG. 14E

52 NRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT
 101 VNVESKDNGK KTEVKIGAKT SVIKEKDGLV VTGKDKGENG SSTDEGEGLV
 151 TAKEVIDAVN KAGWRMKTTH ANGQTGQADK FETVTSGTNV TFASGKGTTA
 201 TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS GWNLDKAVA GSSGKVISGN
 251 VSPSKGKMDE TVNINAGNNI EITRNGKNID IATSMTPQFS SVSLGAGADA
 301 PTLSDGDAL NVGSKKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN
 351 RIDNVDGNAR AGIAQAIATA GLVQAYLPGK SMMAIGGGTY RGEAGYAIGY
 401 SSISDGGNWI IKGTASGNSR GHFGASASVG YQW*

FIG. 14F

50 SANTLKAGDNL KIKQFTYSLK KDLTDLTSVG TEKLSFSANG NKVNITSDTK
 101 GLNFAKETAG TNGDTTVHLN GIGSTLTDR ASDKVVLNAG WNIKGVKNVD
 151 FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS VIKEKDGLV
 201 TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTHA NGQTGQADKF
 251 ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG
 301 WNLDKAVAG SSGKVISGNV SPSKGMDET VNINAGNNIE ITRNGKNIDI
 351 ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK
 401 EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS
 451 MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGy
 501 QW*

FIG. 14G

09771333-071301